RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/229,751 B_

Source: _/600_

Date Processed by STIC: _·7/22/2003_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
        http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry directly to:**
    U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
                Or
    U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. **Federal Express, United Parcel Service, or other delivery service to:** U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 04/24/2003

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/229,751B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics / Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 _____ Invalid Line Length — The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 _____ Misaligned Amino Numbering — The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 _____ Non-ASCII — The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 _____ Variable Length — Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 _____ Skipped Sequences (OLD RULES) — Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 _____ Skipped Sequences (NEW RULES) — Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 _____ Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.

10 _____ Invalid <213> Response — Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 _____ Use of <220> — Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0 "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 _____ Misuse of n — n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

1600

RAW SEQUENCE LISTING   DATE: 07/22/2003
PATENT APPLICATION: **US/09/229,751B**   TIME: 13:49:33

Input Set : **A:\Dosseq.715**
Output Set: **N:\CRF4\07222003\I229751B.raw**

SEQUENCE LISTING
```
  4 (1) GENERAL INFORMATION:
  6       (i) APPLICANT: Turnbough, Charles K
  8      (ii) TITLE OF INVENTION: PEPTIDE LIGANDS THAT BIND TO SURFACES
  9                                OF
 10                                BACTERIAL CELLS
E--> 12    (iii) NUMBER OF SEQUENCES: 26  82 (see p.8)
 14      (iv) CORRESPONDENCE ADDRESS:
 15            (A) ADDRESSEE: Glenna Hendricks
 16            (B) STREET: P.O. Box 2509
 17            (C) CITY: Fairfax
 18            (D) STATE: VA
 19            (E) COUNTRY: USA
 20            (E) ZIP: 22031
 22       (v) COMPUTER READABLE FORM:
 23            (A) MEDIUM TYPE: Floppy disk
 24            (B) COMPUTER: IBM PC compatible
 25            (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 26            (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
 28      (vi) CURRENT APPLICATION DATA:
 29            (A) APPLICATION NUMBER: US/09/229,751B
 30            (B) FILING DATE: 14-Jan-1999
 31            (C) CLASSIFICATION:
 33    (viii) ATTORNEY/AGENT INFORMATION:
 34            (A) NAME: Hendricks, Glenna M
 35            (B) REGISTRATION NUMBER: 32,535
 36            (C) REFERENCE/DOCKET NUMBER: turn
 38      (ix) TELECOMMUNICATION INFORMATION:
 39            (A) TELEPHONE: (703) 425-8405
 40            (B) TELEFAX: (703) 425-8406
```

Does Not Comply
Corrected Diskette Needed

(handwritten) pp 1-8

(handwritten) p.2 (global error)

ERRORED SEQUENCES

```
 64 (2) INFORMATION FOR SEQ ID NO: 2:
 66       (i) SEQUENCE CHARACTERISTICS:
 67            (A) LENGTH: 21 base pairs
 68            (B) TYPE: nucleic acid
 69            (C) STRANDEDNESS: single
 70            (D) TOPOLOGY: unknown
 72      (ii) MOLECULE TYPE: DNA (genomic)
 74     (iii) HYPOTHETICAL: NO
 76      (iv) ANTI-SENSE: NO
```

RAW SEQUENCE LISTING   DATE: 07/22/2003
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Input Set : A:\Dosseq.715
Output Set: N:\CRF4\07222003\I229751B.raw

```
 80      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
E--> 82 AATCATTTTT TGATTAAGCC G          21
W--> 83      21
 85 (2) INFORMATION FOR SEQ ID NO: 3:
 87      (i) SEQUENCE CHARACTERISTICS:
 88          (A) LENGTH: 21 base pairs
 89          (B) TYPE: nucleic acid
 90          (C) STRANDEDNESS: single
 91          (D) TOPOLOGY: unknown
 93      (ii) MOLECULE TYPE: DNA (genomic)
 95     (iii) HYPOTHETICAL: NO
 97      (iv) ANTI-SENSE: NO
101      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
E--> 103 AATCATTTTT TGAGGTCTCC G
W--> 104      21
127 (2) INFORMATION FOR SEQ ID NO: 5:
129      (i) SEQUENCE CHARACTERISTICS:
130          (A) LENGTH: 21 base pairs
131          (B) TYPE: nucleic acid
132          (C) STRANDEDNESS: single
133          (D) TOPOLOGY: unknown
135      (ii) MOLECULE TYPE: DNA (genomic)
137     (iii) HYPOTHETICAL: NO
139      (iv) ANTI-SENSE: NO
143      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
E--> 145 AATCATTTTC TTCCTAAGGT G
W--> 146      21
148 (2) INFORMATION FOR SEQ ID NO: 6:
150      (i) SEQUENCE CHARACTERISTICS:
151          (A) LENGTH: 21 base pairs
152          (B) TYPE: nucleic acid
153          (C) STRANDEDNESS: single
154          (D) TOPOLOGY: unknown
156      (ii) MOLECULE TYPE: DNA (genomic)
158     (iii) HYPOTHETICAL: NO
160      (iv) ANTI-SENSE: NO
164      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
E--> 166 AATCATTTTC TGTTGCCGCC G
W--> 167      21
169 (2) INFORMATION FOR SEQ ID NO: 7:
171      (i) SEQUENCE CHARACTERISTICS:
172          (A) LENGTH: 21 base pairs
173          (B) TYPE: nucleic acid
174          (C) STRANDEDNESS: single
175          (D) TOPOLOGY: unknown
177      (ii) MOLECULE TYPE: peptide
179     (iii) HYPOTHETICAL: NO
181      (iv) ANTI-SENSE: NO
185      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
```

[handwritten: see item 1 on Error Summary Sheet]

[handwritten: same error]

[handwritten: same]

[handwritten: same]

[handwritten: ? This is a DNA sequence.]

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/229,751B

Input Set : A:\Dosseq.715
Output Set: N:\CRF4\07222003\I229751B.raw

```
E--> 187 AATCATTTTC TGCCTCGTTG G                    same
W--> 188     21
     190 (2) INFORMATION FOR SEQ ID NO: 8:
     192     (i) SEQUENCE CHARACTERISTICS:
     193         (A) LENGTH: 21 base pairs
     194         (B) TYPE: nucleic acid
     195         (C) STRANDEDNESS: single
     196         (D) TOPOLOGY: unknown
     198   (ii) MOLECULE TYPE: peptide ?
     200  (iii) HYPOTHETICAL: NO
     202   (iv) ANTI-SENSE: NO
     206    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:   same
E--> 208 AATCATTTTT TGCCTCCTCG G
W--> 209     21
     211 (2) INFORMATION FOR SEQ ID NO: 9:
     213     (i) SEQUENCE CHARACTERISTICS:
     214         (A) LENGTH: 21 base pairs
     215         (B) TYPE: nucleic acid
     216         (C) STRANDEDNESS: single
     217         (D) TOPOLOGY: unknown
     219   (ii) MOLECULE TYPE: DNA (genomic)
     221  (iii) HYPOTHETICAL: NO
     223   (iv) ANTI-SENSE: NO
     227    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:   same
E--> 229 AATCATTTTC TGATGCCGAA G
W--> 230     21
     232 (2) INFORMATION FOR SEQ ID NO: 10:
     234     (i) SEQUENCE CHARACTERISTICS:
     235         (A) LENGTH: 21 base pairs
     236         (B) TYPE: nucleic acid
     237         (C) STRANDEDNESS: single
     238         (D) TOPOLOGY: unknown
     240   (ii) MOLECULE TYPE: DNA (genomic)
     242  (iii) HYPOTHETICAL: NO
     244   (iv) ANTI-SENSE: NO
     248    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:   same
E--> 250 AATCATTTTC TGCCTACTGG G
W--> 251     21
     253 (2) INFORMATION FOR SEQ ID NO: 11:
     255     (i) SEQUENCE CHARACTERISTICS:
     256         (A) LENGTH: 21 base pairs
     257         (B) TYPE: nucleic acid
     258         (C) STRANDEDNESS: single
     259         (D) TOPOLOGY: unknown
     261   (ii) MOLECULE TYPE: DNA (genomic)
     263  (iii) HYPOTHETICAL: NO
     265   (iv) ANTI-SENSE: NO
     269    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
E--> 271 AATCATTTTC TTAAGGGGAC G                       same
```

RAW SEQUENCE LISTING DATE: 07/22/2003
PATENT APPLICATION: **US/09/229,751B** TIME: 13:49:33

Input Set : **A:\Dosseq.715**
Output Set: **N:\CRF4\07222003\I229751B.raw**

```
W--> 272     21
     274 (2) INFORMATION FOR SEQ ID NO: 12:
     276     (i) SEQUENCE CHARACTERISTICS:
     277         (A) LENGTH: 21 base pairs
     278         (B) TYPE: nucleic acid
     279         (C) STRANDEDNESS: single
     280         (D) TOPOLOGY: unknown
     282     (ii) MOLECULE TYPE: DNA (genomic)
     284    (iii) HYPOTHETICAL: NO
     286     (iv) ANTI-SENSE: NO
     290     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
E--> 292 ATTCATTTTC TTCTTTGGCG T
W--> 293     21
     295 (2) INFORMATION FOR SEQ ID NO: 13:
     297     (i) SEQUENCE CHARACTERISTICS:
     298         (A) LENGTH: 21 base pairs
     299         (B) TYPE: nucleic acid
     300         (C) STRANDEDNESS: single
     301         (D) TOPOLOGY: unknown
     303     (ii) MOLECULE TYPE: DNA (genomic)
     305    (iii) HYPOTHETICAL: NO
     307     (iv) ANTI-SENSE: NO
     311     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:
E--> 313 AATCATTTTC TGATTAGGAA G
W--> 314     21
     316 (2) INFORMATION FOR SEQ ID NO: 14:
     318     (i) SEQUENCE CHARACTERISTICS:
     319         (A) LENGTH: 21 base pairs
     320         (B) TYPE: nucleic acid
     321         (C) STRANDEDNESS: single
     322         (D) TOPOLOGY: unknown
     324     (ii) MOLECULE TYPE: DNA (genomic)
     326    (iii) HYPOTHETICAL: NO
     328     (iv) ANTI-SENSE: NO
     332     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:
E--> 334 AATCATTTTC TGCCGACTGC T
W--> 335     21
     379 (2) INFORMATION FOR SEQ ID NO: 17:
     381     (i) SEQUENCE CHARACTERISTICS:
     382         (A) LENGTH: 21 base pairs
     383         (B) TYPE: nucleic acid
     384         (C) STRANDEDNESS: single
     385         (D) TOPOLOGY: unknown
     387     (ii) MOLECULE TYPE: DNA (genomic)
     389    (iii) HYPOTHETICAL: NO
     391     (iv) ANTI-SENSE: NO
     395     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:
E--> 397 ATTCATTTTT TGCCGCAGAA T
W--> 398     21
```

same (handwritten, ×4)

RAW SEQUENCE LISTING   DATE: 07/22/2003
PATENT APPLICATION: **US/09/229,751B**   TIME: 13:49:33

Input Set : **A:\Dosseq.715**
Output Set: **N:\CRF4\07222003\I229751B.raw**

```
 926 (2) INFORMATION FOR SEQ ID NO: 43:
 928      (i) SEQUENCE CHARACTERISTICS:
 929          (A) LENGTH: 7 amino acids
 930          (B) TYPE: amino acid
 931          (C) STRANDEDNESS: single
 932          (D) TOPOLOGY: unknown
 934      (ii) MOLECULE TYPE: peptide
 936     (iii) HYPOTHETICAL: NO
 938      (iv) ANTI-SENSE: NO
 942      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:
E--> 944     Thr-Tyr-Pro-Val-Pro-His-Arg
E--> 945     1                   5
 989 (2) INFORMATION FOR SEQ ID NO: 46:
 991      (i) SEQUENCE CHARACTERISTICS:
 992          (A) LENGTH: 21 base pairs
 993          (B) TYPE: nucleic acid
 994          (C) STRANDEDNESS: single
 995          (D) TOPOLOGY: unknown
 997      (ii) MOLECULE TYPE: DNA (genomic)
 999     (iii) HYPOTHETICAL: NO
1001      (iv) ANTI-SENSE: NO
1005      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:
E--> 1007 ACGCATCGTT TGCCTTCTCG G
W--> 1008     21
1010 (2) INFORMATION FOR SEQ ID NO: 47:
1012      (i) SEQUENCE CHARACTERISTICS:
1013          (A) LENGTH: 21 base pairs
1014          (B) TYPE: nucleic acid
1015          (C) STRANDEDNESS: single
1016          (D) TOPOLOGY: unknown
1018      (ii) MOLECULE TYPE: DNA (genomic)
1020     (iii) HYPOTHETICAL: NO
1022      (iv) ANTI-SENSE: NO
1026      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:
E--> 1028 GTTACTAGTA GGGGGAATGT T
W--> 1029     21
1031 (2) INFORMATION FOR SEQ ID NO: 48:
1033      (i) SEQUENCE CHARACTERISTICS:
1034          (A) LENGTH: 21 base pairs
1035          (B) TYPE: nucleic acid
1036          (C) STRANDEDNESS: single
1037          (D) TOPOLOGY: unknown
1039      (ii) MOLECULE TYPE: DNA (genomic)
1041     (iii) HYPOTHETICAL: NO
1043      (iv) ANTI-SENSE: NO
1047      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:
E--> 1049 AAGCTGTGGG TGATTCCTCA G
W--> 1050     21
1052 (2) INFORMATION FOR SEQ ID NO: 49:
```

delete all dashes — they are invalid
do not use TAB codes between amino acid numbers
use space characters

see item 1 on Error Summary Sheet

same

same

RAW SEQUENCE LISTING   DATE: 07/22/2003
PATENT APPLICATION: **US/09/229,751B**   TIME: 13:49:33

Input Set : **A:\Dosseq.715**
Output Set: **N:\CRF4\07222003\I229751B.raw**

```
        1054      (i) SEQUENCE CHARACTERISTICS:
        1055          (A) LENGTH: 21 base pairs
        1056          (B) TYPE: nucleic acid
        1057          (C) STRANDEDNESS: single
        1058          (D) TOPOLOGY: unknown
        1060     (ii) MOLECULE TYPE: DNA (genomic)
        1062    (iii) HYPOTHETICAL: NO
        1064     (iv) ANTI-SENSE: NO
        1068     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:
E--> 1070 TATTCGCCTC CTCATAGGCA T                         same
W--> 1071      21
        1220 (2) INFORMATION FOR SEQ ID NO: 57:
        1222      (i) SEQUENCE CHARACTERISTICS:
        1223          (A) LENGTH: 21 base pairs
        1224          (B) TYPE: nucleic acid
        1225          (C) STRANDEDNESS: single
        1226          (D) TOPOLOGY: unknown
        1228     (ii) MOLECULE TYPE: DNA (genomic)
        1230    (iii) HYPOTHETICAL: NO
        1232     (iv) ANTI-SENSE: NO
        1236     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:
E--> 1238 TCGTATCCTC CGTATTTTGA T                          same
W--> 1239      21
        1241 (2) INFORMATION FOR SEQ ID NO: 58:
        1243      (i) SEQUENCE CHARACTERISTICS:
        1244          (A) LENGTH: 21 base pairs
        1245          (B) TYPE: nucleic acid
        1246          (C) STRANDEDNESS: single
        1247          (D) TOPOLOGY: unknown
        1249     (ii) MOLECULE TYPE: DNA (genomic)
        1251    (iii) HYPOTHETICAL: NO
        1253     (iv) ANTI-SENSE: NO
        1257     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:
E--> 1259 CTTTTGTCGC CTCTGCATCG T                          same
W--> 1260      21
        1262 (2) INFORMATION FOR SEQ ID NO: 59:
        1264      (i) SEQUENCE CHARACTERISTICS:
        1265          (A) LENGTH: 21 base pairs
        1266          (B) TYPE: nucleic acid
        1267          (C) STRANDEDNESS: single
        1268          (D) TOPOLOGY: unknown
        1270     (ii) MOLECULE TYPE: DNA (genomic)
        1272    (iii) HYPOTHETICAL: NO
        1274     (iv) ANTI-SENSE: NO
        1278     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:
E--> 1280 TTTGATTCTC CGCTTCGTCG G                          same
W--> 1281      21
        1662 (2) INFORMATION FOR SEQ ID NO: 78:
        1664      (i) SEQUENCE CHARACTERISTICS:
```

```
1665            (A) LENGTH: 7 amino acids
1666            (B) TYPE: amino acid
1667            (C) STRANDEDNESS: single
1668            (D) TOPOLOGY: unknown
1670      (ii) MOLECULE TYPE: peptide
1672     (iii) HYPOTHETICAL: NO
1674      (iv) ANTI-SENSE: NO
1678      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:
1680    ·    Phe Asp Ser Pro Leu Arg Arg
1681          1           5
1683 (2) INFORMATION FOR SEQ ID NO: (78):
1685      (i) SEQUENCE CHARACTERISTICS:
1686            (A) LENGTH: 7 amino acids
1687            (B) TYPE: amino acid
1688            (C) STRANDEDNESS: single
1689            (D) TOPOLOGY: unknown
1691      (ii) MOLECULE TYPE: peptide
1693     (iii) HYPOTHETICAL: NO
1695      (iv) ANTI-SENSE: NO
1699      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:
1701          Trp Ser Pro Leu His Lys His
1702          1               5
```

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see p. 8

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(2) INFORMATION FOR SEQ ID NO: 82:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 6 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: unknown
   (ii) MOLECULE TYPE: peptide
  (iii) HYPOTHETICAL: NO
   (iv) ANTI-SENSE: NO
    (v) FRAGMENT TYPE: internal
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:
        Ser Pro Leu Xaa Xaa His
        1   5

last sequence in submitted file